
Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: Tue May 29 11:17:59 EDT 2007

Validated By CRFValidator v 1.0.2

Application No: 10561043 Version No: 1.0

Input Set:

Output Set:

Started: 2007-05-24 22:13:03.583

Finished: 2007-05-24 22:13:04.107

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 524 ms

Total Warnings: 6

Total Errors: 0

No. of SeqIDs Defined: 10

Actual SeqID Count: 10

Error code		Error Description									
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(2)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(3)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(4)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(5)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(6)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(7)

SEQUENCE LISTING

<110> GUPTA, ANTJE ZIMMER, ANKE BOBKOVA, MARIA <120> OXIDOREDUCTASE FROM PICHIA CAPSULATA <130> 4838-002 <140> 10561043 <141> 2007-05-24 <150> 10/561,043 <151> 2005-12-16 <150> PCT/EP04/005831 <151> 2004-05-28 <150> DE 103 27 454.5-41 <151> 2003-06-18 <160> 10 <170> PatentIn Ver. 3.3 <210> 1 <211> 1175 <212> DNA <213> Pichia capsulata <400> 1 cgcggtggcg gccgctctag aactagtgga tcccccgggc tgcaggaatt cggcacgagg 60 atctttctca actacaatgt ctgctctctc caaaacccag gccggttaca tcttcaagaa 120 gggtgccggt cacatcgtca aggccgaggt tccaatcccc aagccaactg gtgcccaatc 180 tettettagg gteaaggetg caggaatgtg ceaetetgae ttgeaegtea ttggagaaae 240 attggaggtc cctaccgatg ggtacgtgct cggtcacgaa attgctggtg aattggtgga 300 gateggagae teggteaace etgaagtttt taaggtggga ggeegttatg etgtteatgg 360 actgaattcg tgtggatcct gtgagatgtg tcgtaccggt catgacaatg actgtactgg 420 aaatgaatcg aaatggtacg gtctgggaat tagtggtggt taccagcagt acctgctggt 480 gccaaattcg caccatctat tgcctattcc agataacgtg tcctacgaag ttgctgctgc 540 cacctctgat gctgtcttga ctccatacca tgctatcaag aattccggag tgactccatc 600 ttctaaggtg ttgatgtttg gtctgggtgg tttgggatcg aacgcacttc agatcctcaa 660 ggcatttgga gcctatgtgg ttgccgttga tgtcaagccc gcatccaaag caattgccga 720 cgaattcaaa geggatgaat tetataeega tateageeaa tettettgga aaceageete 780 gtttgattac tgttttgact tcgtttcgct gcaggtcacc ttcgacatct gccagaagta 840 tatcaagtcc cacggtacca tcttcccagt gggtctgggc tcgagcaagc tgactttcga 900 cttgggaaac ctggcattgc gtgaagtaaa aattgttggt aacttctggg gtacttctca 960 ggaacagatc gaagcaatgg agctggttag ctcgggtagg gtcaagcctc aagttcacac 1020 caccgaactt gaaaaccttc ctgaatcact tgaaaaactg gaggagggta agatcaatgg 1080 aagattggtt atgcttccat gatcacaaac tatttataac gagatacgag aaaaagttta 1140 1175 atatgatgtc gtttttccaa tcaaaagggg ggccc

<210> 2

<211> 366

<212> PRT

<220>

<223> Description of Artificial Sequence: Synthetic Protein

<400> 2

Ala Val Ala Ala Ala Leu Glu Leu Val Asp Pro Pro Gly Cys Arg Asn 1 5 10 15

Ser Ala Arg Gly Ser Phe Ser Thr Thr Met Ser Ala Leu Ser Lys Thr
20 25 30

Gln Ala Gly Tyr Ile Phe Lys Lys Gly Ala Gly His Ile Val Lys Ala 35 40 45

Glu Val Pro Ile Pro Lys Pro Thr Gly Ala Gln Ser Leu Leu Arg Val
50 55 60

Lys Ala Ala Gly Met Cys His Ser Asp Leu His Val Ile Gly Glu Thr 65 70 75 80

Leu Glu Val Pro Thr Asp Gly Tyr Val Leu Gly His Glu Ile Ala Gly
85 90 95

Glu Leu Val Glu Ile Gly Asp Ser Val Asn Pro Glu Val Phe Lys Val
100 105 110

Gly Gly Arg Tyr Ala Val His Gly Leu Asn Ser Cys Gly Ser Cys Glu 115 120 125

Met Cys Arg Thr Gly His Asp Asn Asp Cys Thr Gly Asn Glu Ser Lys 130 135 140

Pro Asn Ser His His Leu Leu Pro Ile Pro Asp Asn Val Ser Tyr Glu 165 170 175

Val Ala Ala Thr Ser Asp Ala Val Leu Thr Pro Tyr His Ala Ile 180 185 190

Lys Asn Ser Gly Val Thr Pro Ser Ser Lys Val Leu Met Phe Gly Leu 195 200 205

Gly Gly Leu Gly Ser Asn Ala Leu Gln Ile Leu Lys Ala Phe Gly Ala 210 215 220

Tyr Val Val Ala Val Asp Val Lys Pro Ala Ser Lys Ala Ile Ala Asp 225 230 235 240

Glu Phe Lys Ala Asp Glu Phe Tyr Thr Asp Ile Ser Gln Ser Ser Trp
245 250 255

Lys Pro Ala Ser Phe Asp Tyr Cys Phe Asp Phe Val Ser Leu Gln Val 260 265 270

Thr Phe Asp Ile Cys Gln Lys Tyr Ile Lys S 275 280	Ser His Gly Thr Ile Phe 285										
Pro Val Gly Leu Gly Ser Ser Lys Leu Thr P 290 295	Phe Asp Leu Gly Asn Leu 300										
Ala Leu Arg Glu Val Lys Ile Val Gly Asn P 305 310 3	Phe Trp Gly Thr Ser Gln 315 320										
Glu Gln Ile Glu Ala Met Glu Leu Val Ser S 325 330	Ser Gly Arg Val Lys Pro 335										
Gln Val His Thr Thr Glu Leu Glu Asn Leu F 340 345	Pro Glu Ser Leu Glu Lys 350										
Leu Glu Glu Gly Lys Ile Asn Gly Arg Leu V 355 360	Val Met Leu Pro 365										
<210> 3 <211> 17 <212> DNA <213> Artificial Sequence											
<220> <223> Description of Artificial Sequence: Synthetic											
Oligonucleotide											
<pre><400> 3 gtaatacgac tataggg 17</pre>											
<210> 4											
<211> 21											
<212> DNA											
<213> Artificial Sequence											
<220>											
<pre><223> Description of Artificial Sequence:</pre>	: Synthetic										
Oligonucleotide	•										
<400> 4											
caattaaccc tcactaaagg g 21											
<210> 5											
<211> 30											
<212> DNA											
<213> Artificial Sequence											
<220>											
<pre><223> Description of Artificial Sequence:</pre>	: Synthetic										
Oligonucleotide	-										
<400> 5											

<400> 5

```
<210> 6
<211> 32
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
     Oligonucleotide
<400> 6
cactgcatgc tgatgtctgc tctctccaaa ac
                                                                   32
<210> 7
<211> 31
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
     Oligonucleotide
<400> 7
cccaagcttt catggaagca taaccaatct t
                                                                   31
<210> 8
<211> 1026
<212> DNA
<213> Pichia capsulata
<400> 8
atgtctgctc tctccaaaac ccaggccggt tacatcttca agaagggtgc cggtcacatc 60
qtcaaqqccq aqqttccaat ccccaaqcca actqqtqccc aatctcttct taqqqtcaaq 120
gctgcaggaa tgtgccactc tgacttgcac gtcattggag aaacattgga ggtccctacc 180
gatgggtacg tgctcggtca cgaaattgct ggtgaattgg tggagatcgg agactcggtc 240
aaccctgaag tttttaaggt gggaggccgt tatgctgttc atggactgaa ttcgtgtgga 300
teetgtgaga tgtgtegtae eggteatgae aatgaetgta etggaaatga ategaaatgg 360
tacggtctgg gaattagtgg tggttaccag cagtacctgc tggtgccaaa ttcgcaccat 420
ctattgccta ttccagataa cgtgtcctac gaagttgctg ctgccacctc tgatgctgtc 480
ttgactccat accatgctat caagaattcc ggagtgactc catcttctaa ggtgttgatg 540
tttggtctgg gtggtttggg atcgaacgca cttcagatcc tcaaggcatt tggagcctat 600
gtggttgccg ttgatgtcaa gcccgcatcc aaagcaattg ccgacgaatt caaagcggat 660
gaattetata eegatateag eeaatettet tggaaaceag eetegtitga tiaetgtitt 720
gacttcgttt cgctgcaggt caccttcgac atctgccaga agtatatcaa gtcccacggt 780
accatettee cagtgggtet gggetegage aagetgaett tegaettggg aaacetggea 840
ttgcgtgaag taaaaattgt tggtaacttc tggggtactt ctcaggaaca gatcgaagca 900
atggagctgg ttagctcggg tagggtcaag cctcaagttc acaccaccga acttgaaaac 960
cttcctgaat cacttgaaaa actggaggag ggtaagatca atggaagatt ggttatgctt 1020
                                                                   1026
ccatga
```

<210> 9 <211> 341

<212> PRT

< 4		9

- Met Ser Ala Leu Ser Lys Thr Gln Ala Gly Tyr Ile Phe Lys Lys Gly
 1 5 10 15
- Ala Gly His Ile Val Lys Ala Glu Val Pro Ile Pro Lys Pro Thr Gly
 20 25 30
- Ala Gln Ser Leu Leu Arg Val Lys Ala Ala Gly Met Cys His Ser Asp 35 40 45
- Leu His Val Ile Gly Glu Thr Leu Glu Val Pro Thr Asp Gly Tyr Val
 50 55 60
- Leu Gly His Glu Ile Ala Gly Glu Leu Val Glu Ile Gly Asp Ser Val
 65 70 75 80
- Asn Pro Glu Val Phe Lys Val Gly Gly Arg Tyr Ala Val His Gly Leu 85 90 95
- Asn Ser Cys Gly Ser Cys Glu Met Cys Arg Thr Gly His Asp Asn Asp 100 105 110
- Cys Thr Gly Asn Glu Ser Lys Trp Tyr Gly Leu Gly Ile Ser Gly Gly
 115 120 125
- Tyr Gln Gln Tyr Leu Leu Val Pro Asn Ser His His Leu Leu Pro Ile 130 135 140
- Pro Asp Asn Val Ser Tyr Glu Val Ala Ala Ala Thr Ser Asp Ala Val
 145 150 155 160
- Leu Thr Pro Tyr His Ala Ile Lys Asn Ser Gly Val Thr Pro Ser Ser 165 170 175
- Lys Val Leu Met Phe Gly Leu Gly Gly Leu Gly Ser Asn Ala Leu Gln
 180 185 190
- Ile Leu Lys Ala Phe Gly Ala Tyr Val Val Ala Val Asp Val Lys Pro 195 200 205
- Ala Ser Lys Ala Ile Ala Asp Glu Phe Lys Ala Asp Glu Phe Tyr Thr 210 215 220
- Asp Ile Ser Gln Ser Ser Trp Lys Pro Ala Ser Phe Asp Tyr Cys Phe 225 230 235 240
- Asp Phe Val Ser Leu Gln Val Thr Phe Asp Ile Cys Gln Lys Tyr Ile 245 250 255
- Lys Ser His Gly Thr Ile Phe Pro Val Gly Leu Gly Ser Ser Lys Leu 260 265 270
- Thr Phe Asp Leu Gly Asn Leu Ala Leu Arg Glu Val Lys Ile Val Gly 275 280 285

Asn Phe Trp Gly Thr Ser Gln Glu Gln Ile Glu Ala Met Glu Leu Val 290 295 300

Ser Ser Gly Arg Val Lys Pro Gln Val His Thr Thr Glu Leu Glu Asn 305 310 315 320

Leu Pro Glu Ser Leu Glu Lys Leu Glu Glu Gly Lys Ile Asn Gly Arg 325 330 335

Leu Val Met Leu Pro 340

<210> 10 <211> 12

<212> PRT

<213> Pichia capsulata

<400> 10

Lys Thr Gln Ala Gly Tyr Ile Phe Lys Lys Gly Ala 1 5 10